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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=1; hr=15; min=18; sec=40; ms=565;]

=====

Reviewer Comments:

<210> 40

<211> 374

<212> PRT

<213> *Pichia pastoris*

<220>

<221> MOD_RES

<222> (176)...(190)

<223> Variable amino acid

<220>

<221> MOD_RES

<222> (202)...(213)

<223> Variable amino acid

<400> 40

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			20				25						30		
Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	His	Ala	Tyr	Ser	Val	Leu	Ser
		35					40					45			
Trp	Tyr	Ser	Asp	Gly	Gly	Glu	Asp	Val	Ser	Phe	Val	Gln	Gln	Ala	Phe
		50				55					60				
Gly	Trp	Leu	Tyr	Leu	Gly	Cys	Leu	Leu	Leu	Ser	Ile	Ser	Ser	Tyr	Phe
65					70					75					80
Phe	Ser	Gly	Leu	Gly	Lys	Ile	Pro	Pro	Val	Tyr	Phe	Val	Leu	Leu	Val
					85				90					95	
Ala	Ser	Lys	Arg	Leu	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn	Asp

Application No: 10500240

Version No: 3.0

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595

Finished: 2008-04-15 16:02:13.772

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms

Total Warnings: 33

Total Errors: 53

No. of SeqIDs Defined: 106

Actual SeqID Count: 106

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (26)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 341	'Xaa' position not defined SEQID (40) POS (160)
E 341	'Xaa' position not defined SEQID (40) POS (161)
E 341	'Xaa' position not defined SEQID (40) POS (162)
E 341	'Xaa' position not defined SEQID (40) POS (163)
E 341	'Xaa' position not defined SEQID (40) POS (164)
E 341	'Xaa' position not defined SEQID (40) POS (165)
E 341	'Xaa' position not defined SEQID (40) POS (166)
E 341	'Xaa' position not defined SEQID (40) POS (167)
E 341	'Xaa' position not defined SEQID (40) POS (168)
E 341	'Xaa' position not defined SEQID (40) POS (169)
E 341	'Xaa' position not defined SEQID (40) POS (170)
E 341	'Xaa' position not defined SEQID (40) POS (171)

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code	Error Description
E 341	'Xaa' position not defined SEQID (40) POS (172)
E 341	'Xaa' position not defined SEQID (40) POS (173)
E 341	'Xaa' position not defined SEQID (40) POS (174)
E 341	'Xaa' position not defined SEQID (40) POS (191)
E 341	'Xaa' position not defined SEQID (40) POS (192)
E 341	'Xaa' position not defined SEQID (40) POS (193)
E 341	'Xaa' position not defined SEQID (40) POS (194)
E 341	'Xaa' position not defined SEQID (40) POS (195) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
W 402	Undefined organism found in <213> in SEQ ID (44)
W 402	Undefined organism found in <213> in SEQ ID (45)
W 402	Undefined organism found in <213> in SEQ ID (46)
W 402	Undefined organism found in <213> in SEQ ID (48)
E 257	Invalid sequence data feature in <221> in SEQ ID (54)
E 257	Invalid sequence data feature in <221> in SEQ ID (56)
E 257	Invalid sequence data feature in <221> in SEQ ID (58)
E 257	Invalid sequence data feature in <221> in SEQ ID (60)
E 257	Invalid sequence data feature in <221> in SEQ ID (62)
E 257	Invalid sequence data feature in <221> in SEQ ID (68)
E 257	Invalid sequence data feature in <221> in SEQ ID (70)
E 257	Invalid sequence data feature in <221> in SEQ ID (72)

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595

Finished: 2008-04-15 16:02:13.772

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms

Total Warnings: 33

Total Errors: 53

No. of SeqIDs Defined: 106

Actual SeqID Count: 106

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (86)
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W 402	Undefined organism found in <213> in SEQ ID (88)
W 402	Undefined organism found in <213> in SEQ ID (90)
W 402	Undefined organism found in <213> in SEQ ID (92)
W 402	Undefined organism found in <213> in SEQ ID (94)

SEQUENCE LISTING

<110> WILET, Stefan
MIELE, Robert G.
NETT, Juergen H.
DAVIDSON, Robert C.

<120> METHODS TO ENGINEER MAMMALIAN-TYPE
CARBOHYDRATE STRUCTURES

<130> GF0022P

<140> 10500240

<141> 2005-03-23

<150> PCT/US02/41510

<151> 2002-12-24

<150> 60/344,169

<151> 2001-12-27

<160> 106

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<211> 35

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<213> Artificial Sequence

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<223> Primer

<400> 1

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<223> Primer

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<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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 <400> 14
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 <400> 21
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 <210> 22
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 <220>
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 <400> 22
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 <213> Saccharomyces cerevisiae

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 His Asp Glu Leu
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 <210> 24
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<220>
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 35 40 45
 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
 50 55 60
 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
 65 70 75 80
 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
 85 90 95
 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
 100 105 110
 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
 115 120 125
 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
 130 135 140
 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
 145 150 155 160
 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
 165 170 175
 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
 180 185 190
 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
 195 200 205
 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
 210 215 220
 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
 225 230 235 240
 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
 245 250 255
 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
 260 265 270
 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
 275 280 285
 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
 290 295 300
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val
 305 310 315 320
 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
 325 330 335
 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
 340 345 350
 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
 355 360 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
 370 375 380
 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
 385 390 395 400
 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa
 405 410 415
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 420 425 430
 Xaa Xaa Xaa Xaa Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
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 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
 450 455

<210> 25

<211> 450

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 25

Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
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 20 25 30
 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 35 40 45
 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
 50 55 60
 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
 65 70 75 80
 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
 85 90 95
 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
 100 105 110
 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
 115 120 125
 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
 130 135 140
 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
 145 150 155 160
 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
 165 170 175
 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
 180 185 190
 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
 195 200 205
 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
 210 215 220
 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
 225 230 235 240
 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
 245 250 255
 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
 260 265 270
 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
 275 280 285
 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His

290	295	300
Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Leu Phe Val		
305	310	315
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His		320
	325	330
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile		335
	340	345
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg		350
	355	360
Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile		365
	370	375
Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr		380
	385	390
Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala		395
	405	410
Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Ala		415
	420	425
Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg		430
	435	440
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	450	455

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<211> 443

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> MOD_RES

<222> (333)...(347)

<223> Variable amino acid

<400> 26

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	20	25
Cys Lys Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys		30
	35	40
Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp		45
	50	55
Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly		60
	65	70
His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp		75
	80	85
His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr		90
	95	100
Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp		105
	110	115
Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val		120
	125	130
Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr		135
	140	145
Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu		150
	155	160
Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met		165
	170	175

180										185										190															
Cys	Cys	Ala	Ser	Tyr	Arg	Val	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe					Cys	Cys	Ala	Ser	Tyr	Arg	Val	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe
195										200										205															
Asn	Asp	Pro	Val	Ala	Met	Val	Leu	Leu	Phe	Leu	Ser	Ile	Asn	Leu	Leu				Asn	Asp	Pro	Val	Ala	Met	Val	Leu	Leu	Phe	Leu	Ser	Ile	Asn	Leu	Leu	
210										215										220															
Leu	Ala	Gln	Arg	Trp	Gly	Trp	Gly	Ser	Leu	Ala	Leu	Val	Ile	Ser	Ala				Leu	Ala	Gln	Arg	Trp	Gly	Trp	Gly	Ser	Leu	Ala	Leu	Val	Ile	Ser	Ala	
225										230										235															
Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu	Leu	Tyr	Phe				Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu	Leu	Tyr	Phe	
245										250										255															
Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala	Asn	Val	Ile				Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala	Asn	Val	Ile	
260										265										270															
Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln	Val	Ala	Val				Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln	Val	Ala	Val	
275										280										285															
Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu	His	Cys	Ala				Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu	His	Cys	Ala	
290										295										300															
Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile	Asn	Trp	Gln				Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile	Asn	Trp	Gln	
305										310										315															
Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	Xaa	Xaa	Xaa	Xaa				Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	Xaa	Xaa	Xaa	Xaa	
325										330										335															
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa				Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
340										345										350															
Pro	Arg	Ile	Leu	Pro	Asp	Leu	Trp	Ser	Ser	Leu	Cys	His	Pro	Leu	Arg				Pro	Arg	Ile	Leu	Pro	Asp	Leu	Trp	Ser	Ser	Leu	Cys	His	Pro	Leu	Arg	
355										360										365															
Lys	Asn	Ala	Val	Leu	Asn	Ala	Asn	Pro	Ala	Lys	Thr	Ile	Pro	Phe	Val				Lys	Asn	Ala	Val	Leu	Asn	Ala	Asn	Pro	Ala	Lys	Thr	Ile	Pro	Phe	Val	
370										375										380															
Leu	Ile	Ala	Ser	Asn	Phe	Ile	Gly	Val	Leu	Phe	Ser	Arg	Ser	Leu	His				Leu	Ile	Ala	Ser	Asn	Phe	Ile	Gly	Val	Leu	Phe	Ser	Arg	Ser	Leu	His	
385										390										395															
Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	His	Trp	Thr	Leu	Pro	Ile	Leu	Ile	Phe				Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	His	Trp	Thr	Leu	Pro	Ile	Leu	Ile	Phe	
405										410										415															
Trp	Ser	Gly	Met	Pro	Phe	Phe	Val	Gly	Pro	Ile	Trp	Tyr	Val	Leu	His				Trp	Ser	Gly	Met	Pro	Phe	Phe	Val	Gly	Pro	Ile	Trp	Tyr	Val	Leu	His	
420										425										430															
Glu	Trp	Cys	Trp	Asn	Ser	Tyr	Pro	Pro	Asn	Ser									Glu	Trp	Cys	Trp	Asn	Ser	Tyr	Pro	Pro	Asn	Ser						
435										440																									

<210> 27
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 27
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 Val Ala Ala Cys Leu Cys Leu Ala Glu Val Gly Ile Thr Phe Trp Val
 20 25 30
 Ile His Arg Val Ala Tyr Thr Glu Ile Asp Trp Lys Ala Tyr Met Ala
 35 40 45
 Glu Val Glu Gly Val Gly Thr Tyr Asp Tyr Thr Gln Leu Gln Gly Asp
 50 55 60
 Thr Gly Pro Leu Val Tyr Pro Ala Gly Phe Val Tyr Ile Phe Met Gly
 65 70 75 80
 Leu Tyr Tyr Ala Thr Ser Arg Gly Thr Asp Ile Arg Met Ala Gln Asn
 85 90 95
 Ile Phe Ala Val Leu Tyr Leu Ala Thr Leu Leu Leu Val Phe Leu Ile
 100 105 110
 Tyr His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met Cys
 115 120 125

[illegible]